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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Connective Tissue Growth Factor - 2

Inventors (please provide full names): Li et al

Point of Contact:
Mona Smith

Technical Info. Specialist
CM1 12C14 Tel: 308-3278

Earliest Priority Filing Date: 7/8/99

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

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part 2

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Vendors and cost where applicable

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USPT,JPAB,EPAB,DWPI,TDBD	(li-haodong.in. or li-h\$.in.) and ctgf	5	<u>L5</u>
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USPT,JPAB,EPAB,DWPI,TDBD	connective adj tissue adj growth adj factor\$	66	<u>L1</u>

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Set	Items	Description
S1	1	CTGF2
S2	1209	CONNECTIVE(W) TISSUE(W) GROWTH(W) FACTOR?
S3	25	S2(S) ISOFORM?
S4	7	RD (unique items)
S5	2	AU=(ADAMS MARK OR ADAMS,M? OR ADAMS M? OR ADAMS, MARK) AND CTGF?
S6	2	RD (unique items)
S7	3	AU=(LI HAODONG OR LI, HAODONG OR LI H? OR LI, H?) AND CTGF
S8	3	RD (unique items)

Tue Jan 9 11:37:33 2001

us-09-348-815-2.rpr

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OM protein - protein search, using sw model
Run on: January 8, 2001, 10:36:00 ; Search time 17.32 Seconds
(without alignments)
1493.658 Million cell updates/sec

Title: US-09-348-815-2
Perfect score: 2115
Sequence: 1 MSSRIARALAVTLLHLTR.....ANEAAFFYRLFNHDKFRD 381

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR66: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1938	91.6	379	2 A35669	gene CYR61 protein
2	1699	80.3	375	2 A41428	CEB-10 protein pre
3	956.5	45.2	348	2 A40578	beta IG-M2 protein
4	952.5	45.0	348	2 A53228	fisp-12 protein pr
5	951	45.0	349	2 A40551	connective tissue
6	855.5	40.4	351	2 S20078	NOV protein - chic
7	834.5	39.5	357	2 I38069	gene novh protein
8	175.5	8.3	1620	2 T27283	hypothetical prote
9	174	8.2	1111	2 T26972	hypothetical prote
10	159	7.5	1700	2 S08167	Balbani ring 3 pr
11	156	7.4	1574	2 T13954	MEGF6 protein - ra
12	153	7.2	837	2 A42112	thrombospondin pr
13	152.5	7.2	1178	1 A39804	zonadhesin - mouse
14	152	7.2	5376	2 T42215	laminin B1k chain
15	147.5	7.0	1170	2 A53612	hypothetical prote
16	145	6.9	601	2 T22025	notch4 - mouse
17	144	6.8	1984	2 T09059	secreted leucine-r
18	142	6.7	1025	2 T42626	mucin - rat
19	141.5	6.7	1034	2 JC5598	hypothetical prote
20	141.5	6.7	1101	2 T16840	mucin, submaxillar
21	141.5	6.7	13288	2 T03099	mucin 2 precursor,
22	141	6.7	3020	2 A49322	mucin protein - fr
23	140.5	6.6	2703	1 A24420	mucin 5AC (clone L
24	139	6.6	1042	2 A57534	cysteine-rich prot
25	138	6.5	251	2 A55035	transmembrane prot
26	138	6.5	2437	2 S18188	notch protein homo
27	136	6.4	2531	2 T42629	tenascin-X - bovin
28	136	6.4	4135	2 T42629	adhesive plaque pr
29	135	6.4	473	2 A56175	

30 135 6.4 1168 2 I56985 kalinin B1 - mou
31 134 6.3 1056 2 A53767 mucin MUC5B, tra
32 134 6.3 3002 2 A47221 fibrillin 1 precu
33 133.5 6.3 1106 2 T13938 gene shuttle craft
34 133.5 6.3 1480 2 A36665 slit protein 1 pre
35 133.5 6.3 1955 1 AGCH agrin precursor -
36 133 6.3 1170 2 A40558 thrombospondin 1 p
37 133 6.3 1296 2 T16859 hypothethical prote
38 133 6.3 2813 1 VWHU von Willebrand fac
39 133 6.3 3106 1 S53868 laminin alpha-2 ch
40 133 6.3 3572 2 T23433 hypothethical prote
41 132.5 6.3 3704 2 T37316 probabable laminin a
42 132.5 6.3 1106 2 T44598 hypothethical prote
43 132.5 6.3 1847 2 T18308 probab vitellologe
44 132.5 6.3 2555 2 A40043 notch protein homo
45 132 6.2 2823 2 T23064 hypothethical prote

ALIGNMENTS

RESULT 1
A35669
gene CYR61 protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 05-Nov-1999
C:Accession: A35669; I48319; S16446
R:O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.
Mol. Cell. Biol. 10, 3569-3577, 1990
A:Title: Expression of cyr61, a growth factor-inducible immediate-early gene.
A:Reference number: A35669; MUID:90287146
A:Accession: A35669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-379 <ORF>
A:Cross-references: GB:M32490; NID:912909; PIDN:AAA37512.1; PID:g309206
A:Note: the authors translated the codon GAT for residue 337 as Gln
R:Latinkic, B.V.; O'Brien, T.P.; Lau, L.F.
Nucleic Acids Res. 19, 3261-3267, 1991
A:Title: Promoter function and structure of the growth factor-inducible immediate ear
A:Reference number: I48319; MUID:91288203
A:Accession: I48319
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-379 <RES>
A:Cross-references: EMBL:X56790; NID:g50632; PIDN:CAA40109.1; PID:g50633
A:Note: the authors did not translate the codon for residue 108
A:Note: the authors translated the codon GAT for residue 337 as Gln
C:Genetics:
A:Gene: CYR61
A:Introns: 21/3; 93/1; 208/1; 279/3
C:Superfamily: von Willebrand factor type C repeat homology
F:99-166/Domain: von Willebrand factor type C repeat homology <YWC>

Query Match 91.6% Score 1938; DB 2; Length 379;
Best Local Similarity 91.4%; Pred. No. 1.2e-135;
Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2;
Qy 1 MSSRIARALAVTLLHLTRLALSTCPAACHCPLAEPKAPGVGLVRDGGCCCKVCAKQL 60
Db 1 MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLAEPKAPGVGLVRDGGCCCKVCAKQL 60
Qy 61 NEDCSKTPQCDHTKGLNFGASSTALKGICRAQSEGRPCYNSRIYQNGSFQPNCKHQ 120
Db 61 NEDCSKTPQCDHTKGLNFGASSTALKGICRAQSEGRPCYNSRIYQNGSFQPNCKHQ 120
Qy 121 CTCIDGAVGCCIPLCPOELSLNLGCPNRLVKYVTCQCEEWVDEDSIKQPMEDQDGLG 180
Db 121 CTCIDGAVGCCIPLCPOELSLNLGCPNRLVKYVTCQCEEWVDEDSIKQPMEDQDGLG 180
Qy 181 KELGFDASEVELTRNELLIAVGKSSKRLPVFGMEPRILYNPL--QGOKCIVOTTSWSQ 238
Db 181 KELGFDASEVELTRNELLIAVGKSSKRLPVFGMEPRILYNPL--QGOKCIVOTTSWSQ 238

Db 179 --LGLDASEVELTRNNELIAGKSSLKRLPVFGTEPRVLFNPLHAHQKQKIVQTTWSQ 236
 QY 239 CSKTCGTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKSPPEVRF 298
 Db 237 CSKSCGTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKSPPEVRF 296
 QY 299 TYAGCLSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNYN 358
 Db 297 TYAGCSSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNYN 356
 QY 359 CPHANEAAFPFYRLFNDIHKFRD 381
 Db 357 CPHNEASFRLYSLFNDIHKFRD 379

RESULT 2
 A41428
 CEF-10 protein precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jul-2000
 R:Simmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R.L.
 Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
 A:Title: Identification of a phorbol ester-repressible v-src-inducible gene.
 A:Reference number: A41428; MUID:89145206
 A:Accession: A41428
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-375 <SIN>
 A:Cross-references: GB:J04496; NID:g211435; PIDN:AAA48661.1; PID:g211436

Query Match 80.3%; Score 1699; DB 2; Length 375;
 Best Local Similarity 81.2%; Pred. No. 4.8e-118;
 Matches 312; Conservative 19; Mismatches 41; Indels 12; Gaps 7;

QY 1 MSSRIARALALVTLHL-TRIAL-STCPAACHCPL-APKCAPGVGLVDRDGGCCCKVCA 59
 Db 1 MGSAGARP-ALAAALCLARLALGSPCAVQCPCAPAAQPCAPGVGLVDRDGGCCCKVCA 59
 QY 60 LNEDCSKTOPCDHTKGLGECNFASSTALKGICRAQSEGRPCPEYNSRIYQNGESFPNC 119
 Db 60 LNEDCSKTOPCDHTKGLGECNFASSTALKGICRAQSEGRPCPEYNSRIYQNGESFPNC 119
 QY 120 QCTCIDGAVGICPLCPQELSLPNLGCPNRLVKTGQCCCEWVCDSDIKDPMEDQGLL 179
 Db 120 QCTCIDGAVGICPLCPQELSLPNLGCPNRLVKTGQCCCEWVCDSDIKDPMEDQGLL 179
 QY 180 KGEIGFDASEVELTRNNELIAGKSSLKRLPVFGTEPRVLFNPLHAHQKQKIVQTTWS 237
 Db 178 SKEFGLDASGELTRNNELIAGKSSLKRLPVFGTEPRVLFNPLHAHQKQKIVQTTWS 232
 QY 238 QCSKTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKSPPEVRF 297
 Db 233 QCSKTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKSPPEVRF 292
 QY 298 FYAGCLSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNY 357
 Db 293 FYAGCSSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNY 352
 QY 358 NCPHANEAAFPFYRLFNDIHKFRD 381
 Db 353 NCPHANEAAFPFYRLFNDIHKFRD 375

RESULT 3
 A40578
 beta IG-M2 protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 05-Nov-1999
 R:Chinn, J.; Neubauer, M.; Purchio, A.F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 293-300, 1991

A:Title: Identification of a gene family regulated by transforming growth factor-beta
 A:Reference number: A40578; MUID:91229699
 A:Accession: A40578
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-348 <BRU>
 A:Cross-references: GB:M80263; NID:g201945; PIDN:AAA73135.1; PID:g201946

Query Match 45.2%; Score 956.5; DB 2; Length 348;
 Best Local Similarity 46.9%; Pred. No. 2.2e-63;
 Matches 179; Conservative 56; Mismatches 106; Indels 41; Gaps 8;

QY 1 MSSRIARALALVTLHL-TRIAL-STCPAACHCPL-APKCAPGVGLVDRDGGCCCKVCA 57
 Db 1 MLASVAGPISLALVLLALCTRPATGQDCSAQCOCACAAEAAPHCAPAGVSLVLDGGCCCRVCA 60
 QY 58 KOLNEDCSKTOPCDHTKGLGECNFASSTALKGICRAQSEGRPCPEYNSRIYQNGESFPNC 117
 Db 61 KOLGELCTERDPCDHPKGLFCDFGSPANKRIGVCTAK-DGAPCVFGSVYRSGESFQSSC 119
 QY 118 KQCTCIDGAVGICPLCPQELSLPNLGCPNRLVKTGQCCCEWVCDSDIKDPMEDQGL 177
 Db 120 KQCTCIDGAVGICPLCPQELSLPNLGCPNRLVKTGQCCCEWVCDSDIKDPMEDQGL 177
 QY 178 LLGKELGFDASEVELTRNNELIAGKSSLKRL-PVFGMEPRILYNPLOGQKCIQVTTSM 236
 Db 169 -----KDRTAGVGPALAAAYRLEDTFGDPDTMM-----RANCLVQTTSM 205
 QY 237 SOCSKTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKSPPEV 296
 Db 206 SACSKTGISTRTVNDNPECLVETRICVPCGPQVYSSLLKGGKCKSKTKSPPEV 265
 QY 297 RFTYAGCLSVKKYRKYPCGSCVDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNY 356
 Db 266 KPELGGCTSVKTYRAKFGVCTDGRCTPQTRTVKMRFCEDGETFSKNVMIQSCCKNY 325
 QY 357 NCPHANEAAFPFYRLFNDI 376
 Db 326 NCPGDNDFESLYRKYMGDM 347

RESULT 4
 A53228
 fisp-12 protein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 05-Nov-1999
 R:Rybeck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
 Cell Growth Differ. 2, 225-233, 1991
 A:Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene
 A:Reference number: A53228; MUID:91363290
 A:Accession: A53228
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <RYS>
 A:Cross-references: GB:M70641; NID:g193313; PIDN:AAA37627.1; PID:g193314
 C:Genetics:
 A:Gene: fisp-12

Query Match 45.0%; Score 952.5; DB 2; Length 348;
 Best Local Similarity 46.6%; Pred. No. 4.4e-63;
 Matches 178; Conservative 57; Mismatches 106; Indels 41; Gaps 8;

QY 1 MSSRIARALALVTLHL-TRIAL-STCPAACHCPL-APKCAPGVGLVDRDGGCCCKVCA 57
 Db 1 MLASVAGPISLALVLLALCTRPATGQDCSAQCOCACAAEAAPHCAPAGVSLVLDGGCCCRVCA 60
 QY 58 KOLNEDCSKTOPCDHTKGLGECNFASSTALKGICRAQSEGRPCPEYNSRIYQNGESFPNC 117
 Db 61 KOLGELCTERDPCDHPKGLFCDFGSPANKRIGVCTAK-DGAPCVFGSVYRSGESFQSSC 119

DR INTERPRO: IPR000867; -
DR INTERPRO: IPR000884; -
DR INTERPRO: IPR001007; -
DR PFAM: PF00007; Cys_knot; 1.
DR PFAM: PF00219; IGFBP; 1.
DR PFAM: PF00090; tsp.1; 1.
DR PFAM: PF00093; vwc; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS01208; VMFC; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 381 CYR61 PROTEIN.
FT DOMAIN 98 164 VMFC.
FT DISULFID 286 360 CTCK.
FT DISULFID 286 323 BY SIMILARITY.
FT DISULFID 303 337 BY SIMILARITY.
FT DISULFID 314 353 BY SIMILARITY.
FT DISULFID 317 355 BY SIMILARITY.
FT DISULFID 322 359 BY SIMILARITY.
FT CONFLICT 210 210 L -> I (IN REF. 4).
FT CONFLICT 220 220 L -> R (IN REF. 4).
SQ SEQUENCE 381 AA; 42026 MW; FC0BD39C078CA0B1 CRC64;

Query Match 100.0%; Score 2115; DB 1; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.9e-154; Indels 0; Gaps 0;
Matches 381; Conservative 0; Mismatches 0;

QY 1 MSSRIARALVVTLLHLTRLALSTCPAACHCPLAPKCAPGVGLVRDGGCGCKVCAKQL 60
DB 1 MSSRIARALVVTLLHLTRLALSTCPAACHCPLAPKCAPGVGLVRDGGCGCKVCAKQL 60
QY 61 NEDCSKTQPCDHTKGLCECNFGASTALGICRAQSEGRPCENSRVYQNGESFPNCKHQ 120
DB 61 NEDCSKTQPCDHTKGLCECNFGASTALGICRAQSEGRPCENSRVYQNGESFPNCKHQ 120
QY 121 CTCIDGAVGCIPLCPQELSPLNLCNPNRLVKTGQCEWVCEDESIKDPMDQDGLLG 180
DB 121 CTCIDGAVGCIPLCPQELSPLNLCNPNRLVKTGQCEWVCEDESIKDPMDQDGLLG 180
QY 181 KELGFDASEVELTRNELLAVKGSLLKPLVFGMEPRILYNPLOGKCIQVQTSWSQCS 240
DB 181 KELGFDASEVELTRNELLAVKGSLLKPLVFGMEPRILYNPLOGKCIQVQTSWSQCS 240
QY 241 KTCGTGISTRTVNDNPECLVETRICVRCPCGQPVYSSLLKKGKCKSKTKKSPVPVRFY 300
DB 241 KTCGTGISTRTVNDNPECLVETRICVRCPCGQPVYSSLLKKGKCKSKTKKSPVPVRFY 300
QY 301 AGCLSVKRYPRKYCGSCVDGRCTTQLTFTVKNRFRCEDETFKSNVMQSKCNYNCP 360
DB 301 AGCLSVKRYPRKYCGSCVDGRCTTQLTFTVKNRFRCEDETFKSNVMQSKCNYNCP 360
QY 361 HANEAAFPYRLFNDIHKFRD 381
DB 361 HANEAAFPYRLFNDIHKFRD 381

RESULT 2
CYR6_MOUSE
ID CYR6_MOUSE STANDARD; PRT; 379 AA.
AC P18406;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-OCT-2000 (Rel. 16, Last annotation update)
DE CYR61 PROTEIN PRECURSOR (3CH61).
GN CYR61 OR IGFBP10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-FIBROBLAST;
RX MEDLINE-90287146; PubMed-2355916;
RA O'Brien T.P., Yang G.P., Sanders L., Lau L.F.;
RT "Expression of cyr61, a growth factor-inducible immediate-early
gene.";
RL Mol. Cell. Biol. 10:3569-3577(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-AJ; TISSUE-EMBRYONIC FIBROBLAST;
RX MEDLINE-91288203; PubMed-2062642;
RA Latinkic B.V., O'Brien T.P., Lau L.F.;
RT "Promoter function and structure of the growth factor-inducible
immediate early gene cyr61.";
RL Nucleic Acids Res. 19:3261-3267(1991).
CC -!- FUNCTION: MAY ACT AS ONE OF THE MANY GROWTH FACTOR-BINDING
PROTEINS: PROMOTES PROLIFERATION, MIGRATION AND ADHESION.
CC -!- TISSUE SPECIFICITY: LOW IN KIDNEY, ADRENAL GLAND, TESTES, BRAIN,
AND OVARY, MODERATE IN HEART, UTERUS, AND SKELETAL MUSCLE, HIGHEST
IN LUNG.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED FROM G(0)/G(1) THROUGH MID-G(1) IN
NORMAL CELLS, AND AT A CONSTANT LEVEL IN RAPIDLY GROWING CELLS.
CC -!- INDUCTION: BY GROWTH FACTORS.
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 VMFC DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTEINE KNOT-LIKE DOMAIN (CTCK).
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M32490; AAA37512.1; -
DR EMBL: X56790; CAA40109.1; -
DR PIR: A35669; A35669.
DR MGD: M8613; CYR61.
DR INTERPRO: IPR000359; -
DR INTERPRO: IPR000867; -
DR INTERPRO: IPR000884; -
DR INTERPRO: IPR001007; -
DR PFAM: PF00007; Cys_knot; 1.
DR PFAM: PF00219; IGFBP; 1.
DR PFAM: PF00090; tsp.1; 1.
DR PFAM: PF00093; vwc; 1.
DR PROSITE: PS00222; IGF_BINDING; 1.
DR PROSITE: PS01185; CTCK_1; 1.
DR PROSITE: PS01225; CTCK_2; 1.
DR PROSITE: PS01208; VMFC; 1.
KW Growth factor binding; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 379 CYR61 PROTEIN.
FT DOMAIN 98 164 VMFC.
FT DISULFID 284 358 CTCK.
FT DISULFID 284 321 BY SIMILARITY.
FT DISULFID 301 335 BY SIMILARITY.
FT DISULFID 312 351 BY SIMILARITY.
FT DISULFID 315 353 BY SIMILARITY.
FT DISULFID 320 357 BY SIMILARITY.
SQ SEQUENCE 379 AA; 41709 MW; FA6B5014B56A8EE9 CRC64;

Query Match 91.6%; Score 1938; DB 1; Length 379;
Best Local Similarity 91.4%; Pred. No. 1.1e-140;
Matches 350; Conservative 9; Mismatches 18; Indels 6; Gaps 2;

QY 1 MSSRIARALVVTLLHLTRLALSTCPAACHCPLAPKCAPGVGLVRDGGCGCKVCAKQL 60
DB 1 MSSRIARALVVTLLHLTRLALSTCPAACHCPLAPKCAPGVGLVRDGGCGCKVCAKQL 60
QY 61 NEDCSKTQPCDHTKGLCECNFGASTALGICRAQSEGRPCENSRVYQNGESFPNCKHQ 120

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Db 61 NEDCSKTPQCDHTKGLFECNFGASSTALKGICRAQSEGRPCENRYIYONGESFQPNCKH 120
QY 121 CTCIDGAVGCIPLCPQELSLNLCNPNRLVKVTGOCCEEWVCDSDIKDPMDQDGLG 180
Db 121 CTCIDGAVGCIPLCPQELSLNLCNPNRLVKVTGOCCEEWVCDSDIKDLDQDGL-- 178
QY 181 KELGFDASEVELTRNNELIAGVGSLLKRLPVFGMEPRILYNPL--QGOKCIVQTTWSQ 238
Db 179 --LGLDASEVELTRNNELIAGVGSLLKRLPVFGTEPRVLFNPLHAGQKCIQVTTWSQ 236
QY 239 CSKTCGTGISTRTVNDNPNCRVLKTRICEVRPCGQPVYSSLLKKGKCKSKTKKSPVPVR 298
Db 237 CSKTCGTGISTRTVNDNPNCRVLKTRICEVRPCGQPVYSSLLKKGKCKSKTKKSPVPVR 296
QY 299 TYAGCLSVKVKYKPCYKCGVDCRCCTPQLTTRTKVNRFCEDGETFSKNVMIQSCRCN 358
Db 297 TYAGCLSVKVKYKPCYKCGVDCRCCTPQLTTRTKVNRFCEDGETFSKNVMIQSCRCN 356
QY 359 CPHANEAFPPYRLFNDIHKFRD 381
Db 357 CPHANEAFPPYRLFNDIHKFRD 379

RESULT 3
CE10_CHICK
ID CE10_CHICK STANDARD; PRT; 375 AA.
AC P19336;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
CE-10 PROTEIN PRECURSOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89145206; PubMed-2537491;
RA Simmons D.L., Levy D.B., Yannoni Y., Erikson R.L.;
RT Identification of a phorbol ester-repressible v-src-inducible gene.;
RL Proc. Natl. Acad. Sci. U.S.A. 86:1178-1182(1989).
CC -!- FUNCTION: PROBABLE SECRETED REGULATORY PROTEIN.
CC -!- INDUCTION: BY V-SRC.
CC -!- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
CC PROTEIN FAMILY. CEF-10/CYR61/CTFG/FISP-12/NOV PROTEIN SUBFAMILY.
CC -!- SIMILARITY: CONTAINS 1 WFEC DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN (CTCK).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J04496; AAA48661.1;
CC PIR; A41428; A41428.
CC INTERPRO; IPR000359;
CC INTERPRO; IPR000867;
CC INTERPRO; IPR000884;
CC INTERPRO; IPR001007;
CC PFAM; PF00007; Cys_knot; 1.
CC PFAM; PF00219; IgFBP; 1.
CC PFAM; PF00090; tsp_1; 1.
CC PFAM; PF00093; vwc; 1.
CC PROSITE; PS00222; IGF_BINDING; 1.
CC PROSITE; PS01185; CTCK_1; 1.
CC PROSITE; PS01225; CTCK_2; 1.
CC PROSITE; PS01208; WFEC; 1.
CC Growth factor binding; signal.
CC SIGNAL 1 22

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FT CHAIN 23 375 CEF-10 PROTEIN.
FT DOMAIN 98 164 WFEC.
FT DISULFID 281 355 CTCK.
FT DISULFID 298 332 BY SIMILARITY.
FT DISULFID 309 348 BY SIMILARITY.
FT DISULFID 312 350 BY SIMILARITY.
FT DISULFID 317 354 BY SIMILARITY.
SQ SEQUENCE 375 AA; 40651 MW; 95F2853BE35D5AE CRC64;

Query Match 80.3%; Score 1699; DB 1; Length 375;
Best Local Similarity 81.2%; Pred. No. 1-7e-122;
Matches 312; Conservative 19; Mismatches 41; Indels 12; Gaps 7;

QY 1 MSSRIARALAVVTLHLRLAL-STCPAACHCPLEAPKAPGVGLVRDGGCGCKVCYCAQ 59
Db 1 MSAGARP-ALAAALICLARLALGSPCAVQCQPAAPQCAPGVGLVRDGGCGCKVCYCAQ 59
QY 60 LNEDCSKTPQCDHTKGLFECNFGASSTALKGICRAQSEGRPCENRYIYONGESFQPNCKH 119
Db 60 LNEDCSKTPQCDHTKGLFECNFGASPAATNGICRAQSEGRPCENRYIYONGESFQPNCKH 119
QY 120 QCTCIDGAVGCIPLCPQELSLNLCNPNRLVKVTGOCCEEWVCDSDIKDPMDQDGL 179
Db 120 QCTCIDGAVGCIPLCPQELSLNLCNPNRLVKVTGOCCEEWVCDSDIKDPMDQDGL 179
QY 180 GRELGFDASEVELTRNNELIAGVGSLLKRLPVFGMEPRILYNPLQOGKQKCIQVTTWS 237
Db 178 SKFGLDASEVELTRNNELIAGVGSLLKRLPVFGMEPRILYNPLQOGKQKCIQVTTWS 237
QY 238 QCSKTCGTGISTRTVNDNPNCRVLKTRICEVRPCGQPVYSSLLKKGKCKSKTKKSPVPVR 297
Db 233 QCSKTCGTGISTRTVNDNPNCRVLKTRICEVRPCGQPVYSSLLKKGKCKSKTKKSPVPVR 297
QY 298 FTYAGCLSVKVKYKPCYKCGVDCRCCTPQLTTRTKVNRFCEDGETFSKNVMIQSCRCN 357
Db 293 FTYAGCLSVKVKYKPCYKCGVDCRCCTPQLTTRTKVNRFCEDGETFSKNVMIQSCRCN 357
QY 358 NCPHANEAFPPYRLFNDIHKFRD 381
Db 353 NCPHANEAFPPYRLFNDIHKFRD 375

RESULT 4
CTGF_MOUSE
ID CTGF_MOUSE STANDARD; PRT; 348 AA.
AC P29268;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR (CTGF) (FISP-12 PROTEIN).
GN CTGF OR FISP12 OR FISP-12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91363290; PubMed-1888698;
RA Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
RT "Structure, mapping, and expression of fisp-12, a growth factor-
RT inducible gene encoding a secreted cysteine-rich protein."
RL Cell Growth Differ. 2:225-233(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-9129699; PubMed-2029337;
RA Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;
RT "Identification of a gene family regulated by transforming growth
RT factor-beta."
RL DNA Cell Biol. 10:293-300(1991).
CC -!- TISSUE SPECIFICITY: TESTIS, SPLEEN, KIDNEY, LUNG, HEART, AND BRAIN
CC -!- (LOWEST LEVEL IN TESTIS AND HIGHEST IN LUNG).
CC -!- INDUCTION: BY GROWTH FACTORS.

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